# RAW SEQUENCE LISTING
# ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH
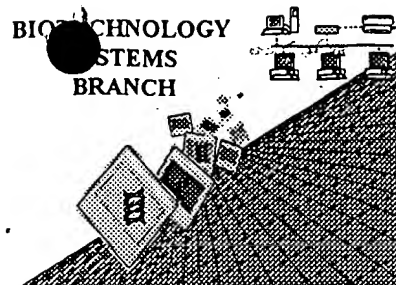
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/ 807, 757_

Source: _PCT09_

Date Processed by STIC: _5-1-01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
## http://www.uspto.gov/web/offices/pac/checker

# Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: *09/807,757* |
|---|---|---|

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of "Artificial" (NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 ✓ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

RAW SEQUENCE LISTING                    DATE: 05/01/2001
PATENT APPLICATION:  US/09/807,757      TIME: 11:30:08

Input Set : A:\Sequence Listing (JB0930.WPD;1).txt
Output Set: N:\CRF3\05012001\I807757.raw

```
 4 <110> APPLICANT: OWENS, Gary K.
 5        MACK, Christopher
 6        BLANK, Randall
 8 <120> TITLE OF INVENTION: Compositions and Methods for Modulating
 9        Expression within Smooth Muscle Cells
12 <130> FILE REFERENCE: 9426-016-228
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/807,757
C--> 14 <141> CURRENT FILING DATE: 2001-04-17
14 <150> PRIOR APPLICATION NUMBER: US60/105,330
15 <151> PRIOR FILING DATE: 1998-10-23
17 <160> NUMBER OF SEQ ID NOS: 18
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

ERRORED SEQUENCES

```
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 5342
23 <212> TYPE: DNA
24 <213> ORGANISM: Rodent
26 <400> SEQUENCE: 1
27 agtactgggt tcaagggaaa gatcctgtct aaaagatcct atggagacaa tcgagggaca     60
28 taaacactat cacccctgg ctttcgcaga cctatatatg cacaagcatg tgcccttgta    120
29 catgtaaatg tgcacacaca gaggcatgca cacctgacat cataccaaag caaagatgaa    180
30 atgaagtaga aatgtcaact ctacatattt tggtggttaa tagttgcatg tgtccagtgg    240
31 ctactgcatc aggagttgct gattctgggc attcctgtca ctaccagagc taactcacca    300
32 ataccatgct aagtcatctc tggaccagag cccagtgagg actaaaatgg tctccagttc    360
33 tcaagggctg aactataaac catcactaaa tcacattgcg gagacattct gtgatgtctg    420
34 tggagcaata cagctggaga tgactcttca gtgtgtgctt atagcttgga tttattttct    480
35 agtttccctg aactgcaacc aagtgaccag atgtacgctc cccaatcagt ccatagctcc    540
36 ttgcatccat ggctgccaac cctggcagtt atctaagcgc tcagtggagc tctgtaaact    600
37 tgtacgcact catccagtgg gcctttctct cccagaagag actggagctg gatataaaat    660
38 ctcaaactct ggctggagag atggctcagt gtttaagagc actgactgct cttccagagt    720
39 tcaaatccca gcaaccacat ggtggcttac agccatctgt aatgatattt gatacctct    780
40 tctggtgtat ctgaagacag ttacactgtg ctcataataa ataaataaat ataagtaaat    840
41 aaataaataa atattttaa aaaccctcaa actcacacat tgtgaccatt aattacttgc    900
42 tcaaaaattg agcaaatcct ccttggttac ttcagattgc tttttgaaat tcttaaaata    960
43 aataaaacaa ctgaaactta ctttcttctt cttgtcataa tattctgatt attgacaaat   1020
44 acaaccagta taaacaaaaa agttataaga ttatcaaagc tcttttcttg gtttttaaag   1080
45 gaattagcat cttgaaatga ccaagacaac actccaacac tcatgaaaca aaacatcagc   1140
46 acagatatcc atgccaggtt ctaaagtaaa aaataaaaca agaaacaaaa acaaaacaaa   1200
47 aaaaaacaaa aaaacaaaga aaaacatgga actttacttt atatgatgcc tatgataaaa   1260
48 ccggttgcat taatcataaa tgtcccatcc tgcctcacaa aatgcagtct ctgtatttga   1320
49 gtgatcagac aatgtatttc tagttggtga aaccagatac agagtagaaa actcttaagc   1380
50 aacacaaaga agccccatta ttatttagca accattacac tcttctaaga gtcaacggtg   1440
51 taattctcaa agacagctat gcgtgcctgg gtgcaggtgg acaccattaa tcaagagcat   1500
52 gagacatggt agcgtgagta gacagctgct ggcattcacc ctgggctttc cctgacatgc   1560
```

```
 53 caacagttca gagccactta tggatccgtc taaaatatct ccatcatgaa ttgaatcaga   1620
 54 accttggctt gcaggaggga agtagagaaa ggtaaagtcg ttgactgtcc attgaagcca   1680
 55 aagagctgat gatgtctttg aagaatggca gggtcacttg atcgctcttt ctgtccagtg   1740
 56 ggctcataaa cacggaggag gatgagcagg cttcatttca acatttcaaa cttcttttac   1800
 57 aatttttttt atgacggggc aatgggtcct ctctgtggcc aaaagacggt ccttaagcat   1860
 58 gatatcaggg gtcagcgata aaccaacaac atgcacgtgg actgtaccta ggggttaacg   1920
 59 cagttacagt gattctgact tctaagttcc tcttagggta acataggctg gtgaatcctg   1980
 60 attacatact tccatatgta atacatacag acttcattga tactacacac agactccaga   2040
 61 ctacatacaa tgtggcttcc ataaatgat cactcctctg cagattcgca ggtgacccaa   2100
 62 gcatcttttg ttataggcta ccttttgcaa cagtgttgcc ttaaagtccc agctagtcag   2160
 63 agacaggccc ttcctcatct caagccctta gctaatggac ccaaaggcta gcctgacagg   2220
 64 aagagctggc atcttctgag gaatgtgcaa accatgcctg cgtctgcttc atgacactag   2280
 65 cccagtgtct gggcatttga gcagttgttc tgagggctca ggatgtttat ccccataagc   2340
 66 agctgaactg cctcctgttt cgagagcaga gcagaggaat gcagtggaag agacccaggc   2400
 67 ctctggccac ccagattaga gagttttgtg ctgaggtccc tatatggttg tgttagagtg   2460
 68 aacggccagc ttcagcctgt ctttgctcct tgtttgggaa gcgagtggga ggggatcaga   2520
 69 ccaggggget atataaccct tcagcattca gcctccccag acaccaccca cccagagtcg   2580
 70 agaagcccag ccagtcgcca tcagggtaag gatgtgactt agagttttcc caggcttttt   2640
 71 aatcatccag tggaaccaga cgttgtctgt agtaatctga atgactaaca tgtttggaat   2700
 72 ttgggaataa agatttatgc tgttaaaatg attgtagctc cttagcttgc atgatttcgt   2760
 73 atctaaacgg gactaaaaat gaatcgtggt ttactggcaa aggagatgga gaggaaatta   2820
 74 aagtttgttc atgcgtggca tctgtgaaat ctgtttacac taaaccaact gctcggatcc   2880
 75 cgcagcctac tataggggag aagtccagcc atctatggta aattatacat ttgtttctac   2940
 76 ttaggtgttg gacacttgtg gatttgtcta tggttcagac ttagtgtgag gactttccat   3000
 77 ctgaccgact acagccgggt taactgaac tggatgtcag gagtgaactg gcgcggttgc   3060
 78 ctgcgctctg gtttttggctg agtggactgc gttgcctctg ggtttccggg gctctaacag   3120
 79 tagacatgta tatcttgtgc ccttacgatt caaacctatg tcattggtca tttgcagcaa   3180
 80 agcatagctc ctctactctc tgcaaagaaa tgaggaagtg tctcattcgg gaaggatctg   3240
 81 attgcgtttc tctgcctcaa gtgtccctct ggcccttag gcagaatctc tgtgggagcc   3300
 82 accccactca ggacttggta acttctgcag ggaaacggag ttttctcgat aagattttcc   3360
 83 tcccctttttg. tgattcatga ctaaatatgg tttgcgtttt gagactcaca aactgggggaa   3420
 84 ggttactgtc ctttcctcct ccctcccctc ccctcttaca attcattttt ggcacaagat   3480
 85 gagctccact gtgctgcacc aaactccccg gcctcgggtg cagttccaaa agcggacgct   3540
 86 ggagcccagt gtgttttacc taattaggaa atgctccctg cttcaaactg aagctgctcc   3600
 87 ttcaggttag ataagagttg caaaccacag cggcagtttc ctctggaaac acaccgacgt   3660
 88 cttctctagt gacgacgctc ctttcaaagc ttattaagac atattttctg gatattttgg   3720
 89 atgaagtaga aatacgtctt tactgaatta gtgattttta cttgcatttt aaaaaaaaac   3780
 90 taggaagctt atttctctga atatactaag gcacaacctt aagtcatcct gcccaacagt   3840
 91 ttatgtgggt tatccttccc cgttttcaaa gggcatccta attccgagtg gtttatctca   3900
 92 tttgcagccc ggatgctatg ttttggacag caggcttcct gtagactctc tgctggtcct   3960
 93 ttgctgctgg ctgcctctgc caatcacctg gctgctgtgc ctctctgtgc tttgagactg   4020
 94 tcttctgagt ctttatcgtc cactggaaag gaagctaaat ataaattcag tgtctgaaag   4080
 95 aagaggcaga gtagagagag gaaagagcaa accaaccaag atcccatttt tccgttcttg   4140
 96 tgaggggaac ccaggcattg aagatttcac tctgatttttg gaggcagggt ttgaaaggaa   4200
 97 accaaaatca caaacagaat ctctgggtaa agacaatagt cacatggtga gatcgacaag   4260
 98 caatgcttgt acaatgccct tgatgtcccc cgaagctgtc gaaaacacaa gcttaaatgt   4320
 99 caattactta aaatgctatt ttaagcccaa aagagtatgt gctcagttag tcaaggttag   4380
100 aagaaatacc agaactcagg ggaggaaaaa atatttataa aacctgatac ttgccacttc   4440
101 caaagaaccc cagtaaatat tttggagaga ataagtaagc tttgggggtg agggagtggg   4500
```

```
      102  gggcaattca  ctttttatta  cggtcatatt  aagtttcttt  ctgtaactta  tcagtcttaa        4560
      103  gtaagaatag  ctattatcat  cctgttgggt  tttcagctta  gcagtgattt  tgattaatga        4620
      104  ggaaatgttg  taaatcctaa  aattgcaaac  tcccccatca  aaaattttca  atccaatatt        4680
      105  ttttactaga  gtaggacttg  gtagcctttc  aacttgtgat  cctcctgcct  cagcttccca        4740
      106  agtggtagga  tcacaggtct  acatcaccac  gcccagtctt  gattcatgtc  taatgccaca        4800
      107  ccagcaccca  agtcttcaga  gacaaaagat  ttttctttta  aacatttaat  atgagcaaac        4860
      108  attttaacat  tctcatatgc  tgcccattat  tccaaaatct  accttttttgg  gggaaaatat        4920
      109  attttaccaa  aaaaaaaagt  gactttggtt  tgatatagat  aacaaacctt  ggtttgatat        4980
      110  agataacaaa  cctttctaga  tagttcttta  acatgtggta  tcactattcc  ctatagacct        5040
      111  gtgttctcca  ctcaggacct  ctcatctgtg  ctctgtggcc  tgttcacaca  ctaatgctct        5100
      112  gccctgcttg  agagtggtaa  aagagcctgt  gagctcctgc  tctttgtgct  gagggcttgt        5160
      113  ggtgctaacc  tggaagtcag  ggtttcagct  catcaaaggc  cttacagtct  ggtgaaagca        5220
      114  tttcaagata  aagagtgtta  gttgagatct  ggggagagcg  tccagctaaa  ataacacaac        5280
      115  agggccaaga  accctggttg  tggttgggag  tgaccgtagg  ctccggccaa  acgcaacctc        5340
E-->  116  ga                                                                           5342 <210>
E-->  117  2
      118  <211> LENGTH: 326
      119  <212> TYPE: DNA
      120  <213> ORGANISM: Rodent
W-->  122  <210> SEQ ID NO:
E-->  122  <400> SEQUENCE: 2
      123  ggaaacggag  ttttctcgat  aagattttcc  tcccctttttg  tgattcatga  ctaaatatgg          60
      124  tttgcgtttt  gagactcaca  aactggggaa  ggttactgtc  ctttcctcct  ccctcccctc         120
      125  ccctcttaca  attcattttt  ggcacaagat  gagctccact  gtgctgcacc  aaactcccccg        180
      126  gcctcgggtg  cagttccaaa  agcggacgct  ggagcccagt  gtgtttttacc  taattaggaa        240
      127  atgctccctg  cttcaaactg  aagctgctcc  ttcaggttag  ataagagttg  caaaccacag        300
      128  cggcagtttc  ctctggaaac  acaccg                                                 326
E-->  130  <210> SEQ ID NO: 3
```

*Enter "hard return" where arrow indicate to move <210> to beginning of next line.*

*This should correct errors shown.*

```
<210> 11
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 11
aattgtttaa                                                    10

<210> 12
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 12
ccctatatca                                                    10

<210> 13
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 13
aataattaaa                                                    10

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 14
ttgctccttg tttgggaagc                                         20

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 15
gaggtcccta tatggttgtg                                         20
```

What is the source of the genetic material in the artificial sequences? Oligonucleotide is not specific enough. See # 12 on the Error Summary Sheet.

Note: This error also occurs in sequences 16, 17, and 18.

**VERIFICATION SUMMARY**          DATE: 05/01/2001
**PATENT APPLICATION:** US/09/807,757    TIME: 11:30:09

Input Set : **A:\Sequence Listing (JB0930.WPD;1).txt**
Output Set: **N:\CRF3\05012001\I807757.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:116 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:5344 SEQ:1
L:116 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:9
M:254 Repeated in SeqNo=1
L:117 M:252 E: No. of Seq. differs, <211>LENGTH:Input:5342 Found:5344 SEQ:1
L:122 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:122 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:2
L:130 M:214 E: (33) Seq.# missing, SEQ ID NO:2